



SEQUENCE LISTING

<110> Sun, Lee-Hwei K
Sun, Bill N
Sun, Cecily R

<120> Fc fusion proteins of human erythropoietin with increased biological activities

<130> 02SUN2001

<140> 09/932812

<141> 2001-08-17

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

cccaagcttg gcgcggagat gggggtgca
29

<210> 2

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 2

cggatccgctc ccctgtcctg caggcct
27

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

gagcgcaaat gttgtgtcga
20

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 4

ggaattctca tttacccgga gacaggga
28

<210> 5

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 5

tggttttctc gatggaggct gggaggcct
29

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 6

aggcctccca gcctccatcg agaaaacca
29

cb
cont

<210> 7
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
cggatccggt ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agcgcaaag
60

ttgtgtcga
69

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
gagtcctaat atggtcccc a
21

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
ggaattctca ttaccacaga gacaggga
28

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10

cctgagttcg cggggggacc a
21

<210> 11

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

gagtccaaat atggtccccc atgccaccca tgcccagcac ctgagttcgc ggggggacca
60

<210> 12

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12

cggatccggt ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agtccaaata
60

tggtcccca
70

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 13

gacaaaactc acacatgccc a
21

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
acctgaagtc gcgggggggac cgt
23

<210> 15
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
gacaaaactc acacatgccc accgtgcccga gcacctgaag tcgcggggggg accgt
55

<210> 16
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16
cggatccggt ggcggttccg gtggaggcgg aagcggcggt ggaggatcag acaaaaactca
60

cacatgcccga
70

<210> 17
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma2 (Figure 2A)

<400> 17

aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc
60

ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac
120

agccgagtcc tggagaggta cctcttggag gccaaaggagg ccgagaatat cacgacgggc
180

tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc
240

tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc
300

ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg
360

gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg
420

cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagtgtgt
480

ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc
540

ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt
600

ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agcgcaaata ttgtgtcgag
660

tgcccaccgt gcccagcacc acctgtggca ggaccgtcag tcttcctctt cccccaaaa
720

cccaaggaca ccctcatgat ctcccggacc cctgaggtca cgtgcgtggg ggtggacgtg
780

agccacgaag accccgaggt ccagttcaac tggtagctgg acggcgtgga ggtgcataat
840

gccaaagaaa agccacggga ggagcagttc aacagcacgt tccgtgtggg cagcgtcctc
900

accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa
960

ggcctcccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca
1020

caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc
1080

tgcctgggtca aaggcttcta cccagcgcac atcgccgtgg agtgggagag caatgggcag
1140

ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcttc
1200

tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcattgctcc
1260

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt
1320

aaatgagaat tc
1332

<210> 18

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2 A)

<400> 18

Met	Gly	Val	His	Glu	Cys	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Leu	Ser	Leu
1				5					10					15	

Leu	Ser	Leu	Pro	Leu	Gly	Leu	Pro	Val	Leu	Gly	Ala	Pro	Pro	Arg	Leu
			20					25						30	

Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu
		35					40					45			

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 210 215 220

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 225 230 235 240

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
420 425 430

Ser Pro Gly Lys
435

<210> 19
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> HuEPO-L-vFc gamma4 (Figure 2B)

<400> 19
aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc
60
ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac
120
agccgagtcc tggagaggta cctcttggag gccaggagg ccgagaatat cacgacgggc
180
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc
240
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc
300
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg
360
gagcccttgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg
420
cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct
480
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc
540
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt
600
ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agtccaaata tgggtcccca
660

tgcccacccat gccagcacc tgagttcgcg gggggacccat cagtcttcct gttcccccca
720

aaacccaagg acactctcat gatctcccg acccctgagg tcacgtgcgt ggtggtggac
780

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat
840

aatgccaaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc
900

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac
960

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag
1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg
1080

acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg
1140

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcccttcttc
1200

ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc
1260

tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg
1320

ggtaaatgag aattc
1335

<210> 20

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B)
)

<400> 20

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 210 215 220

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 245 250 255

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 290 295 300

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 305 310 315 320

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 420 425 430

Leu Ser Leu Gly Lys
 435

<210> 21
 <211> 1329
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-vFc gamma1 (Figure 2C)

<400> 21
 aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc
 60

ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac
 120

agccgagtc tggagaggta cctcttggag gccaaaggagg ccgagaatat caccacgggc
 180

tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc
 240

tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc
 300

ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg
 360

gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg
 420

cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct

480

ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc
540

ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt
600

ggcggttccg gtggaggcgg aagcggcggg ggaggatcag acaaaaactca cacatgccca
660

ccgtgcccag cacctgaagt cgcgggggga ccgtcagtct tcctcttccc cccaaaaccc
720

aaggacaccc tcatgatctc ccggacacct gaggtcacat gcgtgggtgg ggacgtgagc
780

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc
840

aagacaaagc cgcgggagga gcagtacaac agcacgtacc ggggtggtcag cgtcctcacc
900

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaagggtct caacaaagcc
960

ctcccagcct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag
1020

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc
1080

ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg
1140

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac
1200

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg
1260

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa
1320

tgagaattc
1329

<210> 22
 <211> 435
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-vFc gamma1 with a 27-amino acid leader peptide (Figure 2C)
)

<400> 22

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly
 210 215 220

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 225 230 235 240

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 245 250 255

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 260 265 270

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 275 280 285

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 325 330 335

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
340 345 350

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
355 360 365

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
370 375 380

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
385 390 395 400

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
405 410 415

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
420 425 430

Pro Gly Lys
435

<210> 23

$\langle 211 \rangle$	16
-----------------------	----

<212> PRT

<213> Artificial sequence, 16-amino acid peptide linker

<400> 23

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24

$\langle 211 \rangle$ 15

<212> PRT

<213> Human IgG1 hinge sequence

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25
 <211> 10
 <212> PRT
 <213> Truncated human IgG1 hinge sequence
 <400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10

<210> 26
 <211> 232
 <212> PRT
 <213> Human IgG1 Fc with native hinge, CH2 and CH3 domains
 <400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 27

<211> 228

<212> PRT

<213> Human IgG2 Fc with native hinge, CH2 and CH3 domains

<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

35	40	45
His Glu Asp Pro Glu Val	Gln Phe Asn Trp Tyr	Val Asp Gly Val Glu
50	55	60
Val His Asn Ala Lys Thr	Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr	
65	70	75
Phe Arg Val Val Ser Val Leu Thr Val	Val His Gln Asp Trp Leu Asn	
	85	90
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro		
	100	105
Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln		
	115	120
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val		
	130	135
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
	145	150
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
	165	170
Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
	180	185
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
	195	200
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
	210	215
Ser Pro Gly Lys		220

225

<210> 28
 <211> 229
 <212> PRT
 <213> Human IgG4 Fc with native hinge, CH2 and CH3 domains
 <400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

C⁶
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225
